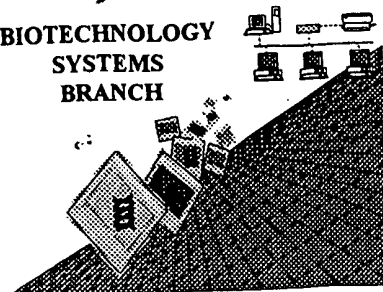


0280

## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/823,886

Source: OIPF

Date Processed by STIC: 4/18/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/823,886

## ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>.-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>.-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>.-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of "Artificial"      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
(NEW RULES)      Valid response is Artificial Sequence.
- 12        Use of <220> Feature      Sequence(s) 16 are missing the <220> Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

Does Not Comply  
Corrected Diskette Needed  
P.6

```

3 <110> APPLICANT: Newell, Martha
4   Berry-Lowe, Sandra
6 <120> TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
8 <130> FILE REFERENCE: C1102/7002
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/823,886
11 <141> CURRENT FILING DATE: 2001-03-30
13 <150> PRIOR APPLICATION NUMBER: US 60/193,533
14 <151> PRIOR FILING DATE: 2000-03-31
W--> 15 <160> NUMBER OF SEQ ID: 16
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 924
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
25 atggggggcc tgacagcctc ggacgtacac cgcaccctgg ggggccagct cttctcagct      60
27 ggaatagcgg cgtgcttggc ggacgtgac accttcccgc tggacacggc caaagtccgg      120
29 ctccagggtcc aaggtgaatg cccgacgtcc agtggtatta ggtataaagg tgcctcgga      180
31 acaatcaccg ctgtggtaaa aacagaaggc cggatgaaac tctacagcgg gctgcctgcg      240
33 gggcttcagc ggcaaatcag ctccgcctct ctcaggatcg gcctctacga cacgggtccag      300
35 gagttcctca ccgagggaag agaaacagca cctagttagt gaagcaagat tttagctggt      360
37 ctaacgactg gaggagtggc agtattcatt gggcaacca cagaggtcgt gaaagtcaga      420
39 cttcaagcac agagccatct ccacggaatc aaacctcgt acacggggac ttataatgcg      480
41 tacagaataa tagcaacaac cgaaggcttg acgggtcttt ggaaagggac tactcccaat      540
43 ctgatgagaa gtgtcatcat caattgtaca gagctagtaa catatgatct aatgaaggag      600
45 gcctttgtga aaaacaacat attagcagat gacgtccct gccactgggt gtcggctctt      660
47 atcgctggat ttgctgcaac agctatgtcc tccccgggtg atgtagttaa aaccagattt      720
49 attaatcttc caccaggaca gtacaaaagt gtgcccaact gtgcaatgaa agtgttcaact      780
51 aacgaaggac caacggcttt cttcaagggt ttggtacctt cttcttgcg acttgatcc      840
53 tggaacgtca ttatgtttgt gtgctttgaa caactgaaac gagaactgtc aaagtcaagg      900
55 cagactatgg actgtgccac ataa                                924
58 <210> SEQ ID NO: 2
59 <211> LENGTH: 307
60 <212> TYPE: PRT
61 <213> ORGANISM: Homo sapiens
W--> 62 <400> SEQUENCE: 2
64 Met Gly Gly Leu Thr Ala Ser Asp Val His Pro Thr Leu Gly Val Gln
65 1                    5                    10                    15
67 Leu Phe Ser Ala Gly Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe
68                20                25                30
70 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro
71            35            40            45
73 Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala
74        50        55        60
76 Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala
77 65                70                75                80
79 Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr

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## RAW SEQUENCE LISTING

DATE: 04/18/2001

PATENT APPLICATION: US/09/823,886

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

80		85		90		95	
82	Asp Thr Val Gln Glu Phe Leu Thr	Ala Gly Lys Glu Thr	Ala Pro Ser				
83		100		105		110	
85	Leu Gly Ser Lys Ile Leu Ala Gly	Leu Thr Thr Gly Gly	Val Ala Val				
86		115		120		125	
88	Phe Ile Gly Gln Pro Thr Glu Val Val	Lys Val Arg Leu Gln Ala Gln					
89		130		135		140	
91	Ser His Leu His Gly Ile Lys Pro Arg Tyr Thr	Gly Thr Tyr Asn Ala					
92	145		150		155		160
94	Tyr Arg Ile Ile Ala Thr Thr Glu Gly Leu Thr	Gly Leu Trp Lys Gly					
95		165		170		175	
97	Thr Thr Pro Asn Leu Met Arg Ser Val Ile Ile	Asn Cys Thr Glu Leu					
98		180		185		190	
100	Val Thr Tyr Asp Leu Met Lys Glu Ala Phe Val	Lys Asn Asn Ile Leu					
101		195		200		205	
103	Ala Asp Asp Val Pro Cys His Leu Val Ser Ala	Leu Ile Ala Gly Phe					
104		210		215		220	
106	Cys Ala Thr Ala Met Ser Ser Pro Val Asp Val	Val Lys Thr Arg Phe					
107	225		230		235		240
109	Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val	Pro Asn Cys Ala Met					
110		245		250		255	
112	Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe	Phe Lys Gly Leu Val					
113		260		265		270	
115	Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val	Ile Met Phe Val Cys					
116		275		280		285	
118	Phe Glu Gln Leu Lys Arg Glu Leu Ser Lys Ser	Arg Gln Thr Met Asp					
119		290		295		300	
121	Cys Ala Thr						
122	305						
124	<210> SEQ ID NO: 3						
125	<211> LENGTH: 1105						
126	<212> TYPE: DNA						
127	<213> ORGANISM: Homo sapiens						
129	<400> SEQUENCE: 3						
130	gttctcttat ctgctcttgt tgctgattaa aggtgccctt	gtctccagtt	tttctccatc	60			
132	tcctgggacg tagcaggaaa tcagcatcat gggtgggttc	aaggccacag	atgtgcccc	120			
134	tactgccact gtgaagtttc ttggggctgg cacagctgcc	tgcatcgag	atctcatcac	180			
136	ctttctcttg gatactgcta aagtccggtt acagatccaa	ggagaaagtc	aggggccagt	240			
138	gcgcgctaca gccagcgccc agtaccgagg tgtgatgggc	accattctga	ccatggtgag	300			
140	tactgagggc ccccgaaagc tctacaatgg gctggttgcc	ggcctgcagc	gccaaatgag	360			
142	ctttgcctct gtccgcatcg gctgtatga ttctgtcaaa	cagttctaca	ccaagggtc	420			
144	tgagcatgcc agcattggga gccgcctcct agcaggcagc	accacaggtg	ccctggctgt	480			
146	ggctgtggcc cagcccacgg atgtggtaaa ggtccgattc	caagctcagg	cccgggctgg	540			
148	aggtggtcgg agataccaaa gcaccgtcaa tgctacaag	accattgccc	gagaggaagg	600			
150	gttccggggc ctctggaaag ggacctctcc caatgttgct	cgtaatgcca	ttgtcaactg	660			
152	tgctgagctg gtgacctatg acctcatcaa ggatgccctc	ctgaaagcca	acctcatgac	720			
154	agatgacctc ccttgccact tcaactctgc ctttggggca	ggcttctgca	ccactgtcat	780			
156	cgctccctct gtagacgtgg tcaagacgag atacatgaac	tctgccctgg	gccagtacag	840			
158	tagcgtgggc cactgtgccc ttaccatgct ccagaaggag	gggccccgag	ccttctacaa	900			

## RAW SEQUENCE LISTING

DATE: 04/18/2001

PATENT APPLICATION: US/09/823,886

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

```

160 aggggttcattg cccctctttc tccgcttgagg ttcctggaac gtggtgatgt tcgtcaccta 960
162 tgagcagctg aaacgagccc tcatggctgc ctgcaattcc cgagaggctc ccttctgagc 1020
164 ctctcctgct gctgacctga tcacctctgg ctttgtctct agccggggcca tgctttcctt 1080
166 ttcttcttcc tttctcttcc ctccg 1105
169 <210> SEQ ID NO: 4
170 <211> LENGTH: 314
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 4
176 Gln Glu Ile Ser Ile Met Val Gly Phe Lys Ala Thr Asp Val Pro Pro
177 1 5 10 15
179 Thr Ala Thr Val Lys Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala
180 20 25 30
182 Asp Leu Ile Thr Phe Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile
183 35 40 45
185 Gln Gly Glu Ser Gln Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr
186 50 55 60
188 Arg Gly Val Met Gly Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro
189 65 70 75 80
191 Arg Ser Leu Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser
192 85 90 95
194 Phe Ala Ser Val Arg Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr
195 100 105 110
197 Thr Lys Gly Ser Glu His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly
198 115 120 125
200 Ser Thr Thr Gly Ala Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val
201 130 135 140
203 Val Lys Val Arg Phe Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg
204 145 150 155 160
206 Tyr Gln Ser Thr Val Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly
207 165 170 175
209 Phe Arg Gly Leu Trp Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala
210 180 185 190
212 Ile Val Asn Cys Ala Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala
213 195 200 205
215 Leu Leu Lys Ala Asn Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr
216 210 215 220
218 Ser Ala Phe Gly Ala Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val
219 225 230 235 240
221 Asp Val Val Lys Thr Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser
222 245 250 255
224 Ser Ala Gly His Cys Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg
225 260 265 270
227 Ala Phe Tyr Lys Gly Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp
228 275 280 285
230 Asn Val Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met
231 290 295 300
233 Ala Ala Cys Thr Ser Arg Glu Ala Pro Phe
234 305 310

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## RAW SEQUENCE LISTING

DATE: 04/18/2001

PATENT APPLICATION: US/09/823,886

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

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236 <210> SEQ ID NO: 5
237 <211> LENGTH: 1132
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 5
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244 ccaccgctgc actgaagccc agggctgtgg agcagcctct ctcttggac ctctctcgg      120
246 ccctaaaggg actgggcaga gccttccagg actatggttg gactgaagcc ttcagacgtg      180
248 cctcccacca tggctgtgaa gtctctgggg gcaggcacag cagcctgttt tgctgacctc      240
250 gttacctttc cactggacac agccaaggtc cgcctgcaga tccaggggga gaaccaggcg      300
252 gtccagacgg cccggctcgt gcagtaccgt ggcgtgctgg gcaccatcct gaccatggtg      360
254 cggactgagg gtccctgcag cccctacaat gggctggtgg ccggcctgca gcgccagatg      420
256 agcttcgcct ccatccgcat cggcctctat gactccgtca agcagggtga ccccccaaa      480
258 ggcgcgga caactccagcct cactaccggt attttgccg gctgcaccac aggagccatg      540
260 gcggtgacct gtgccagcc cacagatgtg gtgaaggctc gatttcaggc cagcatacac      600
262 ctggggccat ccaggagcga cagaaaatac agcgggacta tggacgccta cagaaccatc      660
264 gccagggagg aaggagtcag gggcctgtgg aaaggaaact tgcccaacat catgaggaat      720
266 gctatcgtca actgtgtgta ggtggtgacc tacgacatcc tcaaggagaa gctgctggac      780
268 taccacctgc tcaactgaaa cttccctgct cactttgtct ctgcctttgg agccggcttc      840
270 tgtgccacag tgggtggcctc cccggtggac gtggtgaaga cccggtatat gaactcacct      900
272 ccaggccagt acttcagccc cctcgactgt atgataaaga tgggtggccca ggaggggccc      960
274 acagccttct acaaggggtg agcctcctcc tgcctccagc actccctccc agagaacagg      1020
276 ggcttctttc ttttcgaatg tggctaccgt gggtaaacct gggatgtagc ggtgaagagt      1080
278 acagatgtaa atgccacaaa gaagaagttt aaaaaaacat gcaaaaaaaaa aa      1132
281 <210> SEQ ID NO: 6
282 <211> LENGTH: 284
283 <212> TYPE: PRT
284 <213> ORGANISM: Homo sapiens
286 <400> SEQUENCE: 6
288 Arg Asp Trp Ala Glu Pro Ser Arg Thr Met Val Gly Leu Lys Pro Ser
289 1 5 10 15
291 Asp Val Pro Pro Thr Met Ala Val Lys Phe Leu Gly Ala Gly Thr Ala
292 20 25 30
294 Ala Cys Phe Ala Asp Leu Val Thr Phe Pro Leu Asp Thr Ala Lys Val
295 35 40 45
297 Arg Leu Gln Ile Gln Gly Glu Asn Gln Ala Val Gln Thr Ala Arg Leu
298 50 55 60
300 Val Gln Tyr Arg Gly Val Leu Gly Thr Ile Leu Thr Met Val Arg Thr
301 65 70 75 80
303 Glu Gly Pro Cys Ser Pro Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg
304 85 90 95
306 Gln Met Ser Phe Ala Ser Ile Arg Ile Gly Leu Tyr Asp Ser Val Lys
307 100 105 110
309 Gln Val Tyr Thr Pro Lys Gly Ala Asp Asn Ser Ser Leu Thr Thr Arg
310 115 120 125
312 Ile Leu Ala Gly Cys Thr Thr Gly Ala Met Ala Val Thr Cys Ala Gln
313 130 135 140
315 Pro Thr Asp Val Val Lys Val Arg Phe Gln Ala Ser Ile His Leu Gly
316 145 150 155 160

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## RAW SEQUENCE LISTING

DATE: 04/18/2001

PATENT APPLICATION: US/09/823,886

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

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318 Pro Ser Arg Ser Asp Arg Lys Tyr Ser Gly Thr Met Asp Ala Tyr Arg
319           165           170           175
321 Thr Ile Ala Arg Glu Glu Gly Val Arg Gly Leu Trp Lys Gly Thr Leu
322           180           185           190
324 Pro Asn Ile Met Arg Asn Ala Ile Val Asn Cys Ala Glu Val Val Thr
325           195           200           205
327 Tyr Asp Ile Leu Lys Glu Lys Leu Leu Asp Tyr His Leu Leu Thr Asp
328           210           215           220
330 Asn Phe Pro Cys His Phe Val Ser Ala Phe Gly Ala Gly Phe Cys Ala
331 225           230           235           240
333 Thr Val Val Ala Ser Pro Val Asp Val Val Lys Thr Arg Tyr Met Asn
334           245           250           255
336 Ser Pro Pro Gly Gln Tyr Phe Ser Pro Leu Asp Cys Met Ile Lys Met
337           260           265           270
339 Val Ala Gln Glu Gly Pro Thr Ala Phe Tyr Lys Gly
340           275           280
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343 <211> LENGTH: 6428
344 <212> TYPE: DNA
345 <213> ORGANISM: Solanum tuberosum
347 <400> SEQUENCE: 7
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350 gaaatataaa agagaaagag tggaagaaaa gatgagaaat attatattgt gtatattgag      120
352 taagtgtagt gaacgagaga gttgagacag agaaaatatt ttaagtcttt aactatattc      180
354 actatacaaa ggagaatatt catatgttga aggaaagtgt tcttgtgtgg agttttggac      240
356 tcttcaacta attcagagtt gtacaacgtt attggactat tgtatcctgg agaggacaag      300
358 tcaagagtga tactgctgga tcggtgtaga ttatgccgta gttgacttga atcttcttaa      360
360 agagagttag atattcgtgc ctcagtcctaa aaatttgttt attcattttt gtcattttat      420
362 ttccaactat aatattttgt atttgttgta tattacactg ccttatcatg ataatcatcg      480
364 tgatttctaa ctgatacatg acgtctcaat taaatgtttt ctccaacta aacacatccc      540
366 atatttatat tattcgacat tggttaattt gattatttat cccactttta gcctatgcac      600
368 aggggcgtag ctatgttaaa gtcagggtgt taaattgaat atccttcgtc aaaaactaat      660
370 atcatattta tgtaaaatta tatacgaagt gattaaataa catatttttg acattcttaa      720
372 cagaacaagg tgtgtttgcc caatcgtttc attattctg tcacaattaa caaatctacc      780
374 atgtgaaata ggtgtacttc accatggccc ttgaatgtat gacaagccgt atattcgata      840
376 ggaaagagta acgtttacgc atccttaata aaatgttaga tgatgaatga ggatctaate      900
378 agcatatgtg caaagctcca accaatcatg attatctaata aaagtgtgct ttattcatta      960
380 ttctaaaatt caacaattaa taaaataatt aggtcaaaaag cacatggttg agtggatgag      1020
382 tttgatcaac ttgtaaatat attattgcct ttattcatct ctagcttcat tattattatt      1080
384 ttattaggtt ctattttaatt tctcgtattt gatatttgca ttaaaattca attaatTTTg      1140
386 attcacatga tataaaaccc caatcacact actcgaattt aaaaccttta attaagggga      1200
388 gtaacaattg aataacaaaa aaaaatctgt tgggagtgcc acccccgaat agaccctgta      1260
390 gagcgcgatt caaatttaat cgaaactcta atgtgggctc cgagaaacaa aaaaaaaaaa      1320
392 caattgaata gcaaaggaaa acagagtagt gctgactgag caagcaaaaag cccaattgaa      1380
394 atattagtag taaatgacag caatggccgt tgcgtaggac aagcacagca gcagccccgt      1440
396 tttcgttttt cccaagatct ctctgcaaaa tccttagcct tctttactat ataatagcc      1500
398 ctaaaacccc attttttact ataccatatt cttactcttg ctctgtgatc atcctttctt      1560
400 ctaggagtag ccatctccta gaaccctttt agtttctctt tgtgtttttt tggatcaatt      1620
402 agtcatggga ggaggagatc acggcggaac atcggatatc tcattcgccg gaattatcgc      1680

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<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

*see item 12 on Ewa Summary Sheet*

<220>

<221> Artificial Sequence

<222> (1)..(27)

<400> 16

cttggccatc tcgagcatgc aggcac



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001

TIME: 07:51:32

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:283 W: Missing Blank Line separator, <160> field identifier  
L:62 M:283 W: Missing Blank Line separator, <400> field identifier  
L:663 M:283 W: Missing Blank Line separator, <400> field identifier  
L:744 M:283 W: Missing Blank Line separator, <400> field identifier  
L:806 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:821 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:836 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:851 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:854 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: